



PCT/10

## RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/089,370

DATE: 04/17/2002

TIME: 11:32:11

Input Set : A:\3557-13 seq list.txt

Output Set: N:\CRF3\04172002\J089370.raw

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3 <110> APPLICANT: BASF Aktiengesellschaft  
 5 <120> TITLE OF INVENTION: Plant PRPP amidotransferase  
 7 <130> FILE REFERENCE: NAE991125  
 C--> 9 <140> CURRENT APPLICATION NUMBER: US/10/089,370  
 C--> 10 <141> CURRENT FILING DATE: 2002-03-29  
 12 <160> NUMBER OF SEQ ID NOS: 4  
 14 <170> SOFTWARE: PatentIn Vers. 2.0  
 16 <210> SEQ ID NO: 1  
 17 <211> LENGTH: 1879  
 18 <212> TYPE: DNA  
 19 <213> ORGANISM: Nicotiana tabacum  
 21 <220> FEATURE:  
 22 <221> NAME/KEY: CDS  
 23 <222> LOCATION: (49)..(1767)  
 25 <400> SEQUENCE: 1  
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 27 Met Ala Ala  
 28 1  
 30 acc gtc tcc acc gcc tct gcc gcc gcc acc aat aaa tct cct ctt tcg 105  
 31 Thr Val Ser Thr Ala Ser Ala Ala Ala Thr Asn Lys Ser Pro Leu Ser  
 32 5 10 15  
 34 cag ccc ctc gac aaa ccc ttt tgc tcc cca tct caa aag ctc tta tct 153  
 35 Gln Pro Leu Asp Lys Pro Phe Cys Ser Pro Ser Gln Lys Leu Leu Ser  
 36 20 25 30 35  
 38 tta tcc cct aaa acc ctc cca aaa ccc tat aga act ctc gtc acc gca 201  
 39 Leu Ser Pro Lys Thr Leu Pro Lys Pro Tyr Arg Thr Leu Val Thr Ala  
 40 40 45 50  
 42 tct tcc aaa aac ccc tta aac gac gtc gtt tcg ttt aag aaa tca gct 249  
 43 Ser Ser Lys Asn Pro Leu Asn Asp Val Val Ser Phe Lys Lys Ser Ala  
 44 55 60 65  
 46 gac aat aca ttg gac tcg tat ttt gac gat gaa gac aaa ccc cgt gaa 297  
 47 Asp Asn Thr Leu Asp Ser Tyr Phe Asp Asp Glu Asp Lys Pro Arg Glu  
 48 70 75 80  
 50 gag tgt ggc gtt gtg ggc atc tat ggc gac tca gaa gct tca cgc ctt 345  
 51 Glu Cys Gly Val Val Gly Ile Tyr Gly Asp Ser Glu Ala Ser Arg Leu  
 52 85 90 95  
 54 tgc tat tta gca ctt cac gcg ctt cta cac cgt ggc caa gaa ggc gcc 393  
 55 Cys Tyr Leu Ala Leu His Ala Leu Leu His Arg Gly Gln Glu Gly Ala  
 56 100 105 110 115  
 58 ggc att gtc gcc gtt aac gac gac gtt ctt aag tca att aca ggt gtt 441  
 59 Gly Ile Val Ala Val Asn Asp Asp Val Leu Lys Ser Ile Thr Gly Val  
 60 120 125 130  
 62 ggg tta gta tcc gac gtg ttc aat gag tca aag ctt gac caa ctc cct 489

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63	Gly	Leu	Val	Ser	Asp	Val	Phe	Asn	Glu	Ser	Lys	Leu	Asp	Gln	Leu	Pro	
64				135					140					145			
66	ggt	gac	atg	gca	att	ggc	cac	gtc	tgg	tac	tct	act	gct	ggc	tct	tct	537
67	Gly	Asp	Met	Ala	Ile	Gly	His	Val	Trp	Tyr	Ser	Thr	Ala	Gly	Ser	Ser	
68			150					155					160				
70	atg	tta	aaa	aat	gtt	cag	cct	ttt	gtt	gct	aat	tat	aaa	ttt	ggg	tca	585
71	Met	Leu	Lys	Asn	Val	Gln	Pro	Phe	Val	Ala	Asn	Tyr	Lys	Phe	Gly	Ser	
72		165					170					175					
74	gtt	ggt	gtt	gcc	cat	aat	ggt	aat	tta	gtg	aat	tat	aag	tta	ctg	cgt	633
75	Val	Gly	Val	Ala	His	Asn	Gly	Asn	Leu	Val	Asn	Tyr	Lys	Leu	Leu	Arg	
76	180					185				190					195		
78	ggt	gaa	cta	gaa	gag	aat	ggg	tca	att	ttt	aat	acg	agt	tct	gat	act	681
79	Gly	Glu	Leu	Glu	Glu	Asn	Gly	Ser	Ile	Phe	Asn	Thr	Ser	Ser	Asp	Thr	
80				200					205					210			
82	gaa	gtg	gta	ctt	cac	ctt	att	gct	ata	tcg	aaa	gct	agg	cct	ttt	tta	729
83	Glu	Val	Val	Leu	His	Leu	Ile	Ala	Ile	Ser	Lys	Ala	Arg	Pro	Phe	Leu	
84			215					220					225				
86	ttg	agg	att	gtt	gag	gct	tgt	gaa	aaa	att	gaa	ggt	gct	tat	tct	atg	777
87	Leu	Arg	Ile	Val	Glu	Ala	Cys	Glu	Lys	Ile	Glu	Gly	Ala	Tyr	Ser	Met	
88		230					235					240					
90	gtg	ttt	gtt	act	gag	gat	aag	ttg	gtt	gcc	gta	agg	gat	cct	cat	ggg	825
91	Val	Phe	Val	Thr	Glu	Asp	Lys	Leu	Val	Ala	Val	Arg	Asp	Pro	His	Gly	
92		245				250				255							
94	ttt	agg	cca	ttg	gtt	atg	ggt	agg	aga	agt	aat	ggt	gct	gtt	gtt	ttt	873
95	Phe	Arg	Pro	Leu	Val	Met	Gly	Arg	Arg	Ser	Asn	Gly	Ala	Val	Val	Phe	
96	260				265				270					275			
99	gcg	tcg	gag	acg	tgt	gct	ttg	gat	ttg	att	gag	gct	act	tat	gag	agg	921
100	Ala	Ser	Glu	Thr	Cys	Ala	Leu	Asp	Leu	Ile	Glu	Ala	Thr	Tyr	Glu	Arg	
101				280					285					290			
103	gag	gtg	aat	cct	ggt	gag	gtt	gtt	gtt	gtg	gat	aaa	gat	ggg	gtt	cat	969
104	Glu	Val	Asn	Pro	Gly	Glu	Val	Val	Val	Val	Asp	Lys	Asp	Gly	Val	His	
105			295					300					305				
107	tct	att	tat	ttg	atg	cct	cat	ccc	gag	cat	aaa	tct	tgt	atc	ttt	gag	1017
108	Ser	Ile	Tyr	Leu	Met	Pro	His	Pro	Glu	His	Lys	Ser	Cys	Ile	Phe	Glu	
109		310					315					320					
111	cat	att	tac	ttt	gct	ctg	cct	aat	tcg	gtc	gtg	ttt	ggg	agg	tct	gtg	1065
112	His	Ile	Tyr	Phe	Ala	Leu	Pro	Asn	Ser	Val	Val	Phe	Gly	Arg	Ser	Val	
113		325				330					335						
115	tac	gag	tct	agg	cgt	gct	ttt	gga	gag	att	ctt	gcg	act	gaa	gct	ccc	1113
116	Tyr	Glu	Ser	Arg	Arg	Ala	Phe	Gly	Glu	Ile	Leu	Ala	Thr	Glu	Ala	Pro	
117	340				345				350					355			
119	gta	gaa	tgt	gat	gtt	ggg	ata	gca	gtt	cct	gat	tcg	ggt	atc	gtg	gct	1161
120	Val	Glu	Cys	Asp	Val	Gly	Ile	Ala	Val	Pro	Asp	Ser	Gly	Ile	Val	Ala	
121				360				365						370			
123	gcg	ctc	ggt	tat	gct	gct	aaa	gcg	ggg	gta	ccg	ttt	caa	caa	ggt	ttg	1209
124	Ala	Leu	Gly	Tyr	Ala	Ala	Lys	Ala	Gly	Val	Pro	Phe	Gln	Gln	Gly	Leu	
125			375					380					385				
127	ata	agg	tcg	cat	tat	gtt	ggt	agg	aca	ttt	atc	gag	ccg	tcg	cag	aag	1257
128	Ile	Arg	Ser	His	Tyr	Val	Gly	Arg	Thr	Phe	Ile	Glu	Pro	Ser	Gln	Lys	

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131 ata agg gat ttc ggg gtg aag ctt aag ttg tca cca gtt agg gca tta 1305
132 Ile Arg Asp Phe Gly Val Lys Leu Lys Leu Ser Pro Val Arg Ala Leu
133          405          410          415
135 ttg gag ggg aaa agg gtt gtg gtc gtg gac gat tca atc gtt aga ggg 1353
136 Leu Glu Gly Lys Arg Val Val Val Val Asp Asp Ser Ile Val Arg Gly
137 420          425          430          435
139 acg acc tcg tcc aag att gtg agg ttg ttg aag gag gcg ggt gcg aaa 1401
140 Thr Thr Ser Ser Lys Ile Val Arg Leu Leu Lys Glu Ala Gly Ala Lys
141          440          445          450
143 gag gtt cat atg agg att gca agc cca cca att ata gct tct tgt tat 1449
144 Glu Val His Met Arg Ile Ala Ser Pro Pro Ile Ile Ala Ser Cys Tyr
145          455          460          465
148 tat gga gtg gat act cct agt tca gat gag ctg ata tca aat agg atg 1497
149 Tyr Gly Val Asp Thr Pro Ser Ser Ser Asp Glu Leu Ile Ser Asn Arg Met
150          470          475          480
152 agt gtg gag gag att aag gag ttc att gga tcg gat tcg ctt gct ttt 1545
153 Ser Val Glu Glu Ile Lys Glu Phe Ile Gly Ser Asp Ser Leu Ala Phe
154          485          490          495
156 ctg cca atg gat agc ttg aat aag ttg tta ggc aat gat tct aaa agc 1593
157 Leu Pro Met Asp Ser Leu Asn Lys Leu Leu Gly Asn Asp Ser Lys Ser
158 500          505          510          515
160 ttt tgc tat gct tgc ttt tcg ggc aat tac ccg gtc gag ccg acg ggt 1641
161 Phe Cys Tyr Ala Cys Phe Ser Gly Asn Tyr Pro Val Glu Pro Thr Gly
162          520          525          530
164 aag gtt aaa agg att ggg gat ttc atg gat gat gga tta agt gga gat 1689
165 Lys Val Lys Arg Ile Gly Asp Phe Met Asp Asp Gly Leu Ser Gly Asp
166          535          540          545
168 atg gat tcc att gat ggt ggt tgg cta cca gga agt agt agg gtt caa 1737
169 Met Asp Ser Ile Asp Gly Gly Trp Leu Pro Gly Ser Ser Arg Val Gln
170          550          555          560
172 aag act atc ttg aat gaa gtt aga acc ggc taaactttct tttccatggt 1787
173 Lys Thr Ile Leu Asn Glu Val Arg Thr Gly
174          565          570
176 tgcttttagtt ttgtcttttg atttctaattg cttgactata gaaattataa gtttcaatga 1847
178 agtctctttt tctaaaaaaa aaaaaaaaaa aa 1879
181 <210> SEQ ID NO: 2
182 <211> LENGTH: 573
183 <212> TYPE: PRT
184 <213> ORGANISM: Nicotiana tabacum
186 <400> SEQUENCE: 2
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188 1 5 10 15
190 Pro Leu Ser Gln Pro Leu Asp Lys Pro Phe Cys Ser Pro Ser Gln Lys
191 20 25 30
193 Leu Leu Ser Leu Ser Pro Lys Thr Leu Pro Lys Pro Tyr Arg Thr Leu
194 35 40 45
197 Val Thr Ala Ser Ser Lys Asn Pro Leu Asn Asp Val Val Ser Phe Lys
198 50 55 60

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200 Lys Ser Ala Asp Asn Thr Leu Asp Ser Tyr Phe Asp Asp Glu Asp Lys
201 65 70 75 80
203 Pro Arg Glu Glu Cys Gly Val Val Gly Ile Tyr Gly Asp Ser Glu Ala
204 85 90 95
206 Ser Arg Leu Cys Tyr Leu Ala Leu His Ala Leu Leu His Arg Gly Gln
207 100 105 110
209 Glu Gly Ala Gly Ile Val Ala Val Asn Asp Asp Val Leu Lys Ser Ile
210 115 120 125
212 Thr Gly Val Gly Leu Val Ser Asp Val Phe Asn Glu Ser Lys Leu Asp
213 130 135 140
215 Gln Leu Pro Gly Asp Met Ala Ile Gly His Val Trp Tyr Ser Thr Ala
216 145 150 155 160
218 Gly Ser Ser Met Leu Lys Asn Val Gln Pro Phe Val Ala Asn Tyr Lys
219 165 170 175
221 Phe Gly Ser Val Gly Val Ala His Asn Gly Asn Leu Val Asn Tyr Lys
222 180 185 190
224 Leu Leu Arg Gly Glu Leu Glu Glu Asn Gly Ser Ile Phe Asn Thr Ser
225 195 200 205
227 Ser Asp Thr Glu Val Val Leu His Leu Ile Ala Ile Ser Lys Ala Arg
228 210 215 220
230 Pro Phe Leu Leu Arg Ile Val Glu Ala Cys Glu Lys Ile Glu Gly Ala
231 225 230 235 240
233 Tyr Ser Met Val Phe Val Thr Glu Asp Lys Leu Val Ala Val Arg Asp
234 245 250 255
236 Pro His Gly Phe Arg Pro Leu Val Met Gly Arg Arg Ser Asn Gly Ala
237 260 265 270
239 Val Val Phe Ala Ser Glu Thr Cys Ala Leu Asp Leu Ile Glu Ala Thr
240 275 280 285
242 Tyr Glu Arg Glu Val Asn Pro Gly Glu Val Val Val Val Asp Lys Asp
243 290 295 300
246 Gly Val His Ser Ile Tyr Leu Met Pro His Pro Glu His Lys Ser Cys
247 305 310 315 320
249 Ile Phe Glu His Ile Tyr Phe Ala Leu Pro Asn Ser Val Val Phe Gly
250 325 330 335
252 Arg Ser Val Tyr Glu Ser Arg Arg Ala Phe Gly Glu Ile Leu Ala Thr
253 340 345 350
255 Glu Ala Pro Val Glu Cys Asp Val Gly Ile Ala Val Pro Asp Ser Gly
256 355 360 365
258 Ile Val Ala Ala Leu Gly Tyr Ala Ala Lys Ala Gly Val Pro Phe Gln
259 370 375 380
261 Gln Gly Leu Ile Arg Ser His Tyr Val Gly Arg Thr Phe Ile Glu Pro
262 385 390 395 400
264 Ser Gln Lys Ile Arg Asp Phe Gly Val Lys Leu Lys Leu Ser Pro Val
265 405 410 415
267 Arg Ala Leu Leu Glu Gly Lys Arg Val Val Val Val Asp Asp Ser Ile
268 420 425 430
270 Val Arg Gly Thr Thr Ser Ser Lys Ile Val Arg Leu Leu Lys Glu Ala
271 435 440 445
273 Gly Ala Lys Glu Val His Met Arg Ile Ala Ser Pro Pro Ile Ile Ala

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274      450      455      460
276 Ser Cys Tyr Tyr Gly Val Asp Thr Pro Ser Ser Asp Glu Leu Ile Ser
277 465      470      475      480
279 Asn Arg Met Ser Val Glu Glu Ile Lys Glu Phe Ile Gly Ser Asp Ser
280      485      490      495
282 Leu Ala Phe Leu Pro Met Asp Ser Leu Asn Lys Leu Leu Gly Asn Asp
283      500      505      510
285 Ser Lys Ser Phe Cys Tyr Ala Cys Phe Ser Gly Asn Tyr Pro Val Glu
286      515      520      525
288 Pro Thr Gly Lys Val Lys Arg Ile Gly Asp Phe Met Asp Asp Gly Leu
289      530      535      540
291 Ser Gly Asp Met Asp Ser Ile Asp Gly Gly Trp Leu Pro Gly Ser Ser
292 545      550      555      560
295 Arg Val Gln Lys Thr Ile Leu Asn Glu Val Arg Thr Gly
296      565      570
299 <210> SEQ ID NO: 3
300 <211> LENGTH: 1869
301 <212> TYPE: DNA
302 <213> ORGANISM: Nicotiana tabacum
304 <220> FEATURE:
305 <221> NAME/KEY: CDS
306 <222> LOCATION: (25)..(1743)
308 <400> SEQUENCE: 3
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310      Met Ala Ala Thr Val Ser Thr Ala Ser
311      1      5
313 gcc gcc gcc acc aac aaa tat cct ctt tca cag ccc ctt gac aaa ccc 99
314 Ala Ala Ala Thr Asn Lys Tyr Pro Leu Ser Gln Pro Leu Asp Lys Pro
315 10      15      20      25
317 ttt tgc tcc cta tct caa aag ctc tta tct tta tcc cct aaa acc cat 147
318 Phe Cys Ser Leu Ser Gln Lys Leu Leu Ser Leu Ser Pro Lys Thr His
319      30      35      40
321 cct aaa ccc tac aga act ctc atc acc gcc tct tcc aaa aac ccc tta 195
322 Pro Lys Pro Tyr Arg Thr Leu Ile Thr Ala Ser Ser Lys Asn Pro Leu
323      45      50      55
325 aac gac gtc att tcg ttt aag aaa tca gct gac aat acc ttg gac tcc 243
326 Asn Asp Val Ile Ser Phe Lys Lys Ser Ala Asp Asn Thr Leu Asp Ser
327      60      65      70
329 tat ttt gac gat gac gat aaa ccc cgt gaa gag tgc ggc gtt gtg ggc 291
330 Tyr Phe Asp Asp Asp Asp Lys Pro Arg Glu Glu Cys Gly Val Val Gly
331      75      80      85
333 atc tat ggc gac tca gaa gct tca cgc ctt tgc tat tta gca ctt cac 339
334 Ile Tyr Gly Asp Ser Glu Ala Ser Arg Leu Cys Tyr Leu Ala Leu His
335 90      95      100      105
337 gcg ctt caa cac cgt ggc caa gaa ggc gcc ggc att gtc gcc gtt aac 387
338 Ala Leu Gln His Arg Gly Gln Glu Gly Ala Gly Ile Val Ala Val Asn
339      110      115      120
341 gac gac gtt ctt aag tca att aca ggt gtt ggg tta gta tcc gac gtg 435
342 Asp Asp Val Leu Lys Ser Ile Thr Gly Val Gly Leu Val Ser Asp Val

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**VERIFICATION SUMMARY**

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Input Set : A:\3557-13 seq list.txt

Output Set: N:\CRF3\04172002\J089370.raw

L:9 M:270 C: Current Application Number differs, Replaced Application Number

L:10 M:271 C: Current Filing Date differs, Replaced Current Filing Date